



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/236,995
Art Unit / Team No.: 01PE
Date Processed by STIC: 2/10/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/236,995

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.
- 7 Wrong Designation Sequence(s) contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (1) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xl) SEQUENCE DESCRIPTION: SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of N's or Xaa's Use of N's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
 (Sec. 1.823 of new Sequence Rules)
- 13 Wrong Format File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the
"Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620
applies to applications filed on or after July 1, 1998.
AKS-Biotechnology Systems Branch- 7/10/98

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/236,995

DATE: 02/10/1999
TIME: 15:39:15

Input Set: I236995.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

see p. 5, too

Does Not Comply
Corrected Diskette Needed

pp 3, 4

1 <110> APPLICANT: Mahajan, Pramod B.
2 Zuo, Zhuang
3 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and Its Uses
4 <130> FILE REFERENCE: 5718-34, 035718-174234
5 <140> CURRENT APPLICATION NUMBER: US/09/236,995
6 <141> CURRENT FILING DATE: 1999-01-26
7 <150> EARLIER APPLICATION NUMBER: 60/072,785
8 <151> EARLIER FILING DATE: 1998-01-27
9 <160> NUMBER OF SEQ ID NOS: 5
10 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 2949
13 <212> TYPE: DNA
14 <213> ORGANISM: Zea mays
15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (1)..(2949)
18 <400> SEQUENCE: 1
19 atg gcg gcg ccg cca aag gcg tgg aag gcg gag tat gcc aag tct ggg 48
20 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
21 1 5 10 15
22 cgg gcc tcg tgc aag tca tgc cgg tcc cct atc gcc aag gac cag ctc 96
23 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
24 20 25 30
25 cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg 144
26 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
27 35 40 45
28 atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata aaa 192
29 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
30 50 55 60
31 tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa 240
32 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
33 65 70 75 80
34 gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt aca agt tct 288
35 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
36 85 90 95
37 aca gct gct cct cct gag aaa tgt aca att gag att gct cca tct gcc 336
38 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
39 100 105 110
40 cgt act tca tgt aga cga tgc agt gaa aag att aca aaa gga tcg gtc 384
41 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
42 115 120 125
43 cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt ata cca tgg 432
44 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp

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Input Set: I236995.RAW

| | | | | |
|----|---|------|-----|--|
| 45 | 130 | 135 | 140 | |
| 46 | tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca act gtt gag | 480 | | |
| 47 | Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu | | | |
| 48 | 145 150 155 160 | | | |
| 49 | aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag aga acc atg | 528 | | |
| 50 | Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met | | | |
| 51 | 165 170 175 | | | |
| 52 | ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa aat aag ggt | 576 | | |
| 53 | Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly | | | |
| 54 | 180 185 190 | | | |
| 55 | tcc aag cgc aag aaa agt gaa aat gat att gat agc tac aaa tcc gcc | 624 | | |
| 56 | Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala | | | |
| 57 | 195 200 205 | | | |
| 58 | agg tta gat gaa agt aca tct gaa ggt aca gtg cga aac aaa ggg caa | 672 | | |
| 59 | Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln | | | |
| 60 | 210 215 220 | | | |
| 61 | ctt gta gac cca cgt ggt tcc aat act agt tca gct gat atc caa cta | 720 | | |
| 62 | Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu | | | |
| 63 | 225 230 235 240 | | | |
| 64 | aag ctt aag gag caa agt gac aca ctt tgg aag tta aag gat gga ctt | 768 | | |
| 65 | Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu | | | |
| 66 | 245 250 255 | | | |
| 67 | aag act cat gta tcg gct gct gaa tta agg gat atg ctt gag gct aat | 816 | | |
| 68 | Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn | | | |
| 69 | 260 265 270 | | | |
| 70 | ggg cag gat aca tca gga cca gaa agg cac cta ttg gat cgc tgt gcg | 864 | | |
| 71 | Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala | | | |
| 72 | 275 280 285 | | | |
| 73 | gat gga atg cta ttt gga gcg ctg ggt cct tgc cca gtc tgt gct aat | 912 | | |
| 74 | Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn | | | |
| 75 | 290 295 300 | | | |
| 76 | ggc atg tac tat tat aat ggt cag tac caa tgc agt ggt aat gtg tca | 960 | | |
| 77 | Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser | | | |
| 78 | 305 310 315 320 | | | |
| 79 | gag tgg tcc aag tgt aca tac tct gcc aca gaa cct gtc cgc gtt aag | 1008 | | |
| 80 | Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys | | | |
| 81 | 325 330 335 | | | |
| 82 | aag aag tgg caa att cca cat gga aca aag aat gat tac ctt atg aag | 1056 | | |
| 83 | Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys | | | |
| 84 | 340 345 350 | | | |
| 85 | tgg ttc aaa tct caa aag gtt aag aaa cca gag agg gtt ctt cca cca | 1104 | | |
| 86 | Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro | | | |
| 87 | 355 360 365 | | | |
| 88 | atg tca cct gag aaa tct gga agt aaa gca act cag aga aca tca ttg | 1152 | | |
| 89 | Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu | | | |
| 90 | 370 375 380 | | | |
| 91 | ctg tct tct aaa ggg ttg gat aaa tta agg ttt tct gtt gta gga caa | 1200 | | |
| 92 | Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln | | | |
| 93 | 385 390 395 400 | | | |
| 94 | tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa ctt gct ggt | 1248 | | |

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DATE: 02/10/1999
TIME: 15:39:15

Input Set: I236995.RAW

| | | |
|----------|--|---------------------------|
| 95 | Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly | |
| 96 | | 405 410 415 |
| 97 | gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca | 1296 |
| 98 | Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala | |
| 99 | | 420 425 430 |
| 100 | tgt ggt gag ctc gac aat gaa aat gct gaa gtc agg aaa gca agg agg | 1344 |
| 101 | Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg | |
| 102 | | 435 440 445 |
| 103 | ctg aag ata cca att gta agg gag ggt tac att gga gaa tgt gtt aaa | 1392 |
| 104 | Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys | |
| 105 | | 450 455 460 |
| 106 | aga aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta gag | 1440 |
| 107 | Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu | |
| 108 | | 465 470 475 480 |
| 109 | tcc tca aaa ggc mgt act gtc act gtt aaa gtt aag ggc cga agt gct | 1488 |
| 110 | Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala | |
| 111 | | 485 490 495 |
| 112 | tgt tca tya agt cct cyg gtt tgc aag aat act gct cac att cct tra | 1536 |
| 113 | Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa | |
| 114 | | 500 505 510 |
| W--> 115 | gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn | 1584 <i>see item 10</i> |
| 116 | Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa | <i>Eira</i> |
| 117 | | 515 520 525 |
| W--> 118 | cac mag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat | 1632 <i>summary sheet</i> |
| 119 | His Xaa Val Xaa Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp | |
| 120 | | 530 535 540 |
| 121 | gat ggg tct gag tgc tac gta ttt cgt aag tgg gga cgg gtt ggg agt | 1680 |
| 122 | Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser | |
| 123 | | 545 550 555 560 |
| 124 | gag aaa att gga ggg caa aaa ctg gag gag atg tca aaa act gag gca | 1728 |
| 125 | Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala | |
| 126 | | 565 570 575 |
| 127 | atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac tca tgg | 1776 |
| 128 | Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp | |
| 129 | | 580 585 590 |
| 130 | gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct ggg aga ttt | 1824 |
| 131 | Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe | |
| 132 | | 595 600 605 |
| 133 | tac cca ctt gat gtt gat tat ggt gtt aag aaa gca cca aaa cgg aaa | 1872 |
| 134 | Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys | |
| 135 | | 610 615 620 |
| 136 | gat atc agt gaa atg aaa agt tct ctt gct cct caa ttg cta gaa ctc | 1920 |
| 137 | Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu | |
| 138 | | 625 630 635 640 |
| 139 | atg aag atg ctt ttc aat gtg gag aca tat aga gct gct atg atg gaa | 1968 |
| 140 | Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu | |
| 141 | | 645 650 655 |
| 142 | ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra | 2016 |
| 143 | Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa | |
| 144 | | 660 665 670 |

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W-->

145 aat att gag raa gga ttt gaa gca tta act krg rta cmg rat tta ttt 2064
 146 Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
 147 675 680 685
 148 gaa gga cac cgc tta tca agc act ggc ttg ttr gag aaa gct naa ttg 2112
 149 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
 150 690 695 700
 151 ttg ytg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc 2160
 152 Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
 153 705 710 715 720
 154 ata tta tac ggg atg agg atg att tca tat tca aag gcg aaa atg ctt 2208
 155 Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
 156 725 730 735
 157 gaa gct ctg cag gat att gaa att gct tca aag ata gtt ggc ttc gat 2256
 158 Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
 159 740 745 750
 160 agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac tgt 2304
 161 Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
 162 755 760 765
 163 gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att gag 2352
 164 Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
 165 770 775 780
 166 cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tgg ctg 2400
 167 Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu
 168 785 790 795 800
 169 gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa ctt aat aag 2448
 170 Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys
 171 805 810 815
 172 tac tca aga tat aaa aat aat ctg cat aac aag atg cta tta tgg cac 2496
 173 Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His
 174 820 825 830
 175 ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta aga 2544
 176 Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg
 177 835 840 845
 178 att gca cct cct gag gca cct gtt act ggc tat atg ttc ggc aaa ggc 2592
 179 Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
 180 850 855 860
 181 ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat gtg 2640
 182 Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val
 183 865 870 875 880
 184 gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta 2688
 185 Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu
 186 885 890 895
 187 gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca 2736
 188 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
 189 900 905 910
 190 aga ggg aag cat tgg acc aag gga tta ggc aaa acc gtg cca ctg gag 2784
 191 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
 192 915 920 925
 193 tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag 2832
 194 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/236,995

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TIME: 15:39:15

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195          930          935          940
196    ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac    2880
197    Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
198    945          950          955          960
199    atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg    2928
200    Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val
201          965          970          975
202    cgt ttc cat cac aag agg tag    2949
203    Arg Phe His His Lys Arg
204          980
205    <210> SEQ ID NO 2
206    <211> LENGTH: 982
207    <212> TYPE: PRT
208    <213> ORGANISM: Zea mays
209    <400> SEQUENCE: 2
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211    1          5          10          15
212    Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
213    20          25          30
214    Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
215    35          40          45
216    Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
217    50          55          60
218    Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
219    65          70          75          80
220    Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
221    85          90          95
222    Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
223    100          105          110
224    Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
225    115          120          125
226    Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
227    130          135          140
228    Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
229    145          150          155          160
230    Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
231    165          170          175
232    Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
233    180          185          190
234    Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
235    195          200          205
236    Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
237    210          215          220
238    Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
239    225          230          235          240
240    Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
241    245          250          255
242    Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn .
243    260          265          270
244    Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I236995.RAW

| Line | Error/Warning | Original Text |
|------|---------------------------------------|---|
| 115 | W "N" or "Xaa" used: Feature required | gra tgg gaa aag cat ata caa tgc amc ctt a |
| 118 | W "N" or "Xaa" used: Feature required | cac nag gtg tgy aca ggc tac tat gta ctc c |
| 148 | W "N" or "Xaa" used: Feature required | gaa gga cac cgc tna tca agc act ggc ttg t |
| 270 | W "N" or "Xaa" used: Feature required | Ser Ser Lys Gly Xaa Thr Val Thr Val Lys V |
| 272 | W "N" or "Xaa" used: Feature required | Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn T |
| 274 | W "N" or "Xaa" used: Feature required | Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu L |
| 276 | W "N" or "Xaa" used: Feature required | His Xaa Val Xaa Thr Gly Tyr Tyr Val Leu G |
| 292 | W "N" or "Xaa" used: Feature required | Phe Glu Xaa Asn Met Ser Glu Met Pro Leu G |
| 294 | W "N" or "Xaa" used: Feature required | Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr X |
| 296 | W "N" or "Xaa" used: Feature required | Glu Gly His Arg Xaa Ser Ser Thr Gly Leu X |
| 298 | W "N" or "Xaa" used: Feature required | Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu S |